



FILING DATE: 1997-05-16  
 APPLICATION NUMBER: 60/044,031  
 FILING DATE: 1997-05-06  
 APPLICATION NUMBER: 60/066,009  
 FILING DATE: 1997-11-14  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kenley K. Hoover  
 REGISTRATION NUMBER: 40,302  
 REFERENCE/DOCKET NUMBER: PB369  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 167:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19031 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 167:  
 US-09-070-927A-167

Alignment Scores:  
 Pred. No.: 0.00357 Length: 19031  
 Score: 139.50 Matches: 140  
 Percent Similarity: 31.38% Conservative: 95  
 Best Local Similarity: 18.69% Mismatches: 247  
 Query Match: 4.13% Indels: 267  
 Gaps: 31

US-09-677-653a-50 (1-647) x US-09-070-927A-167 (1-19031)  
 QY 19 AsnValArgValSerIleAsnThrValThrValAsnGlyArgArgAsnGlnArgArg 38  
 DB 4462 AACCGGAAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4506  
 QY 39 ThrGlyArgGlnValSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGln 58  
 DB 4507 -----ATCACACCGCGCCACAGGTTTCACCCCAAGGTAAACCGGTGATTACA 4554  
 QY 59 SerLeuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer----- 73  
 DB 4555 ACC-----GACGCTACACTTCAACACAGACGACACTTACACACACTTACACACAGGC 4611  
 QY 74 -----MetProGluPheArgAsnThrAlaAlaGlyLysIleAspLeuAspSerAspSer 91  
 DB 4612 GGTAAAGACCTCAAGATTCAAGGTGGTACAAAGGCAAGTCCACTCAACATGAGACA 4671  
 QY 92 IleGlyTrpTrpPheLysTrpLeuAspProAlaGlyAlaThrGluSerAlaArgAlaVal 111  
 DB 4672 ACT----- 4674  
 QY 112 GlyIuTrpSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArg 131  
 DB 4675 -----ACCAACCGCGCAAGTTATCAAGTACCTACGATGACATATGATTTGAAT 4725  
 QY 132 GluIleTrpAsnGluGlnCysProValValThrAspValSerValProLeuAsp----- 149  
 DB 4726 GTGGTGTATGAGAAGAAAGTACGACAGTATCCATGATGCAATGAACTTGTG 4785  
 QY 150 -----GlyArgGlnTrpSerLeu 155  
 DB 4786 AATGAAAAAGCGGGCTTTCACACCGGCTTAACCTTTAGTGAAGTACATGCGCAA 4845  
 QY 156 SerIlePheSerPheProMetPheArgThrAlaTrpValAlaValAlaAsnValGluAsn 175  
 DB 4846 AGTACGAGTGGCTAC-----TTAAGAACCGATTATATGACGTGACCTCAAAAAATTAAT 4899  
 QY 176 -----LysGluMetSerLeuAspValValAlaAsnAspLeu 186  
 DB 4900 GGTATAGGCATATACGTAGTATGATATATGATGATGATGATGATGATGATGATGAT 4959  
 QY 187 IleGluTrpLeuAsn----- 191

DB 4960 TTGAAAAAATATATATATGACCAACCAATCAGTGTACCAACAGATTACATTAATGTT 5019  
 QY 191 ----- 191  
 DB 5020 GATTAATTTAGCCATGCAACCAACTAATAATATGTTGACAGCATTTCAATTAGACACAGCT 5079  
 QY 192 -----AsnLeuAlaAspTrpArgTrpValVal----- 200  
 DB 5080 CAAAGTAGCAATGTGAATTCCTATATATATGTTACACGACAAATAGTCACGTGTTTC 5139  
 QY 201 -----AspSerGluGlnTrpIleAsn 207  
 DB 5140 GACCCAAATGTACACACAGAGAGTTGACTTATGACAAATCTCTTAACCTTGAAT 5199  
 QY 208 PheThrAsnAspThrTrpTrpTrp----- 215  
 DB 5200 TTTGATTCAGATGCGCACTATTTTCTTAATGCAAAATATAGACTTTTTCACGCAATTGA 5259  
 QY 216 -----ValArgIleArgValLeuArgProThrTrpAspVal----- 227  
 DB 5260 GGTATATAGTGCACACAGAGAGTTACTATCTCTGTAATATGTTCTTTTAAACGCCAA 5319  
 QY 228 ProAspProThrGluGlyLeuValArgThrValSerAspTrpArgLeuThrTrpLysAla 247  
 DB 5320 CCGCGGATTAAGTCAAAACTTGTCT-----TACAAAGTCACTCGCAACAA 5364  
 QY 248 IleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGln 267  
 DB 5365 GTCAAC-----GAAAACCTTGCGAT-----GTCAACGGTGGC 5397  
 QY 268 TyrAlaLeuThrProThrSerLeuProGlnTrpAspValSerGluValAlaLeuHis 287  
 DB 5398 AAAATACGTACGACCAACAGGCTTCACCA-----GTAACCAATACCAATGAAAC 5448  
 QY 288 ThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeu----- 300  
 DB 5449 AGTAAACCTTC-----AAGTACACAGCGCAAAAGTTTACACGCACTACTACAGGT 5505  
 QY 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyLysThrAlaProAlaGlyThrPro 318  
 DB 5506 GCGAAAGTATATACGTTCCAAAGGTGGTATTAAGGAAACCAAGCAGATGAGTTG 5562  
 QY 319 AlaTrpGluGlnAlaSerSerGlyLysTrpThrTrpArgHisAsnGlyThrTrpPhe 338  
 DB 5563 ----- 5577  
 QY 339 ProAlaGlySerValSerTrpValLeuProGluGlyPheAlaLeuGluArgTrpPro 358  
 DB 5578 CCAACGTTCAATGCGAC-----TTTGAATGCG 5604  
 QY 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378  
 DB 5605 AATGACGATATACCGCCCTATATAGAAAGAAATACCAACGCTAGTCACTTAAT 5664  
 QY 379 AlaValAspGluValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPhe 398  
 DB 5665 CGACCAAAAGAGTATGATATACCAATGTAATGTGACAAACAGATCAAGAT 5724  
 QY 399 ThrValArgValProProSerAsnAlaTrpThrAsnThrValPheArgAsnThrLeuLeu 418  
 DB 5725 ACTAGCAAGACACCC-----TTACAAATATCTCACTTGC 5757  
 QY 419 GluThrArgProSer-----SerArgArgLeuGluLeuPro-----MetProProAlaAsp 435  
 DB 5758 AAAAAAGGCCCAATTTGGTCTGACCTGTGACAGATCCGACCTTTATGGAAGTGACACA 5817  
 QY 436 PheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGlnThrLeu 455  
 DB 5818 GAAGGAGAAACGACAAATCAATCCCA-----GTAATATAGTACCTTTGACAGAGGGGTT 5874  
 QY 456 GlyCysTrpLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475  
 DB 5875 -----CCTTACCAAAATGCGTTCCTATGCGC 5901

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QY 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyrGluArgThr 490
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Db 5902 AAAAAAGTTTCAGTTCCTTCAACAACTCCGCAACAGGAAACCAACACTGTTTGAAA 5961
QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMetSerThrAla 510
      :|:|:|:|:|:|
Db 5962 GCAGAGTTGTAGTATTTGGTATTTAAAGATAGTACAGTGCATTAACCTTC----- 6012
QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrIlystrIlyGlnGly 530
      :|:|:|:|:|:|
Db 6013 -----GTGAGATTCTGTCCAAAATGATCAAGAGATGTCACACCAACAGCAGGAGGC 6063
QY 531 TTPGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisIleGlyLeuLeu 550
      :|:|:|:|:|:|
Db 6064 TTCATCAGTGCACAACTTCGAC-----TTCGGCCAAGTGGCGCTTCGAGAACTAAG 6117
QY 551 LysAsnGluGluIleLeuCysLeuAlaAsp-----560
      :|:|:|:|:|:|
Db 6118 CAACACACAGCTTGAAACAGCCGCGATTTACTACGTACAGGACACAGCAATCCGTAT 6177
QY 561 -----AspLeuAlaThrArgLeuThrGlyValTyr 570
      :|:|:|:|:|:|
Db 6178 CTGCGGATTAGAAAAAGCAACCCAAATGAGCTTAAACAGCGCACTGTCACAAACAAA 6237
QY 571 ProAlaThrAspAsnPhe-----AlaAlaAlaValSer 581
      :|:|:|:|:|:|
Db 6238 TCAGCGACAGACAGCTTGCTTACAGGACCGCTTATTTAGGGCGCGCTGCTCT 6297
QY 582 AlaPheAlaAlaAsnMetLeuSerSerValIleLysSerGlu-----AlaThrSerSer 599
      :|:|:|:|:|:|
Db 6298 ACCTTACCAATTACATCAACCAACCGAGTGAATAATACGGTCCGTACACAGACTGCC 6357
QY 600 IleIleLysSerValGlyIleThrAla 608
      :|:|:|:|:|:|
Db 6358 ATTAGCTTAAACAGCCAAACACACAGCA 6384

RESULT 2
US-09-070-927A-150
; Sequence 150. Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;           Patrick J. Dillon
;           Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 962
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302

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; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11739 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-070-927A-150

Alignment Scores:
Pred. No.: 0.0206 Length: 11739
Score: 129.00 Matches: 160
Percent Similarity: 31.86% Conservative: 107
Best Local Similarity: 19.09% Mismatches: 255
Query Match: 3.82% Indels: 317
DB: 10 Gaps: 43

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Db 9107 ACGAATCGTAGTTCCTAATAGCGGAGTAAAGACACCAATATATGTTAGTAAACATCTTGTA 9166
QY 28 ThrValAsnGlyArgArgAsnGlnArg-----36
      :|:|:|:|:|:|
Db 9167 GGAAACACAGGACAGTTCATTAAGGAATTCGTCTACTATTAATTAATTAATTTAT 9226
QY 37 -----ArgArgThrGlyArgGlnValSerProPheAsp 47
      :|:|:|:|:|:|
Db 9227 TACAAAAGCTTTATGAGAAATTTGTTAATPAGTACGGACAAATAATACACCACTCA 9286
QY 48 AsnPheThrAlaAlaIleAsnIleAspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhe 67
      :|:|:|:|:|:|
Db 9287 GGATTCACACAGGAAGGAAGGAGCTT-----ATTAAATAGTAAACGTAACCTTTT 9337
QY 68 ProAlaAsnIleSerSerMetProGlu-----Phe 77
      :|:|:|:|:|:|
Db 9338 AAACAAAGT---GGCACCTTCCAGATACCTATCAAGCAGAGCGCAAAACCTAATAGTTC 9394
QY 78 ArgAsnThrAlaLysGlyLysIle-----85
      :|:|:|:|:|:|
Db 9395 AAAGTTGGTACAAAGCAAAACCAACCAACACCTTACCACCAACCAACCAACGAC 9454
QY 86 -----AspLeu-----87
      :|:|:|:|:|:|
Db 9455 TATCGGTGACTTATTAACATGATGATTTGACGGTGGTGTATGAGAGATGAGTTT 9514
QY 88 ---AspSerAspSerIleGlyTyrPheLysTyrLeuAspProAlaGlyAlaThrGlu 106
      :|:|:|:|:|:|
Db 9515 TTTGACTCCAGCGCTGACTCATCAATTCGGGTGTGGAGCTGCAAGAGTA 9574
QY 107 SerAlaArgAlaValGly---GluTyrSerLysIleProAspGlyLeuValLysPheSer 125
      :|:|:|:|:|:|
Db 9575 GATGCTTCAACAATGGGTGACTTATGACAAATGGCGTGGGAGATGTTGTAACAATAAT 9634
QY 126 ValAsp-----AlaGlu 129
      :|:|:|:|:|:|
Db 9635 GTCAATGACTGGAAAAACATCAGTCTTGAAAAAGTCAGTTCACCAACCAACCAACAT 9694
QY 130 IleArgGluIleTyr-----AsnGluGluCysProValValThrAspValSerValPro 147
      :|:|:|:|:|:|
Db 9695 TTGAAGAAATTCCTATCTCGCAATCTCTTGAATATCTGAGATGATGAGTACAA--- 9751
QY 148 LeuAspGlyArgGlnThrPheSerLeuSerIlePheSerPhePromet-----162
      :|:|:|:|:|:|
Db 9752 -----CAATATAGTCGGCTAATTTAACCTTTTACCTGCCCAATATCATATGGG 9799
QY 163 -----PheArgThrAlaTyrValAlaValAlaAsn 172
      :|:|:|:|:|:|

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Db	9800	AAAATCAGTGTATTATACAAAGAGTGTACTTTTGATGACGCTACTG---	-TTTCCAAT	9856
Oy	173	ValGluAsnLysGluMetSerLeuAspValValAsnAspLeuIleGluThrPheAsnAsn		192
Db	9857	ATCCAAATAAATAATAGTTTCAGAACACATCTGTTGAAGGCTTACACAAA	-----AAT	9907
Oy	193	LeuAlaAspTrp		196
Db	9908	CTTTCTAGCTGGTTGAACTAAAGAAAGAGTGGAAACCAATCGTTGTTTAAACAAACGG		9967
Oy	197	-----	ArgThrValValAspSer	202
Db	9968	ATTCCAGCAGCAACCAATGCATGTCTTACGGTCCCTACTTGGCAGAGATTGCTATTAAT	10022	
Oy	203	GluGlnTrpIleAsnPheThrAsnAspThrThrTyrrValArgIleArgValLeuArg		222
Db	10028	CCCGATCTGATA-----TCAAAATACAGCGCTATATATGTA-----	-ATAGATAAA	10072
Oy	223	ProThrTyrrAspValProAspProThrGluGlyLeuValArgThrValSerAspTrpArg		242
Db	10073	CCTGCTAC-----	-TACTAT	10087
Oy	243	LeuThrTyrrLysAlaIleThr-----	-CysGluAlaAsnMet	254
Db	10088	TTAACCAACCCGAAAGTCCACCAAACTCGTAGACACAAAGGCGTCCAAATTCACACA	10147	
Oy	255	ProThrLeuValAspGlnGlyPheThrPileGlyGlyGlnTrpAlaLeuThrPro-ThrSe		274
Db	10148	CCAAACA-----GGTTTACCCCAAGAAACAAACAGCGATTACAGTACGCCCA	10195	
Oy	274	IleuProGlnTrpAspValSerGluAlaGlyThrAlaLeuHisThrLeuThrPheAlaArg		294
Db	10196	TACACCTTCA--AACAAACAGGTAACCTTCACTGATCACTACCAACAAACGCGGTAAAGAC	10253	
Oy	294	oSerSerAlaAlaAlaLeuAlaPheValTrpAlaGlyLeuProGlnGlyGlyThrAlaPr		314
Db	10253	TACAAGTCAAAAGCT-----	-GATACA	10274
Oy	314	oAlaGlyThrProAlaTrpGlu-----	-GlnAlaSerSerGlyGlyTrpIle	329
Db	10275	-AAGGAAACCCAAACAC-GACCCCTTTAACACAGCAAGAAACACCAAGTTATGGG--GT	10329	
Oy	329	uThrTrpArgHisAsnGly-----	-ThrThrPheThr	339
Db	10330	AACCTATATATGATTAATGATGATTTGAATCTGGTATGTAAGAAGTAACAGCTATTTATTC	10389	
Oy	339	oAlaGlySerValSerTyrrValLeuProGlnGlyPheAlaLeuGluArgTyrrAspProAs		359
Db	10390	AGGGTTCATATGGCAATTTGTTGATGACAAACAGCAAGCTTTACTAATTCGCTAATCT	10449	
Oy	359	nasPaspIySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArg-----		376
Db	10450	TTCTGAATAATTACTGAGTTTCTCAGAAAGACAGCACTACTGTTTTGAACGAAGG	10509	
Oy	377	-----GlnValAlaValAspGluValValThrAsnAsnProAlaGlyGlu		392
Db	10510	CGCCTTTTACCCAATGTAGAGTAAGCGGATCCAAACAGTCAATAATAGTATAG--	10564	
Oy	392	yGlySerAlaProThrPheThrValArgValPro-----	-ProSe	405
Db	10565	-----ATTGAACAACAGAGTAGTGTTGCGATACCAATAATATTATTGGACAGCCATGCGCTGC	10620	
Oy	405	rAsn-----	-AlaTyrrThrAsnThrValPheArgAsnThrLeu-----	417
Db	10621	TGACATTGCTATATAGAGGTACGACATTTAATTAATCACTTGATATTACCAATCAATGAATA	10680	
Oy	418	-----LeuGluThrArgProSerSerArgArgLeu-----		427
Db	10681	TGTTGACAAAGATAGAACTACTGACACGCACACTCATATGTACATGTATATACGAGATTTC	10740	
Oy	428	-GluLeuProMetProProAlaAspPheGlyGlnThrValAlaAsnAsnProLysIleGlu		447
Db	10741	GGACATTTGGGGGCAACCAACCAAAATGCTTCTTCAGCAACAAATTAAT-----CCTATTGA	10794	

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QY 447 ucInserLeuLysGluThrLeuGlycysrtyLeuValHisSerLysMetArgAsnPr 467
Db 10795 TAAACACATTGTTAAAGCAACAGATPAACACTTTGGCGAATAAATATTTGGGGAATG 10854
QY 467 oValPheGln-----LeuThrProAlaSerSerPheGlyAl 479
Db 10855 AACGTTTCGCATATAGTCCCAAAATGTATATTGTTAGCAAGAAAGTGGAGTTTTCAG 10914
QY 479 aVal--SerPheAsn--AsnProGlyTyrGluArgThrArgAspLeuProAspTyrTh 497
Db 10915 ATTATTCGGGTTGTATGTGACTCCAGACTACAGCAACAAACC-----GTAAACTACAA 10965
QY 497 rclYLeuArgAspSerPheAspGlnAsmMetSerThrAla----- 510
Db 10966 AGTCAACCGGTAAACAAGTACCAGAAAACCTTTGATGCGCAACGGTCCAAATACACGC 11023
QY 510 ----- 510
Db 11026 ACCAACAGGCTTCACCCACAGGACACAAATATACCATTGACTACCAACACTTCAAGTAC 11085
QY 511 -ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyGlnGl 530
Db 11086 AGCCCAAAAGCCTTCGCACGCACTTATCCACAGGTGGCAAGACCTATCTTCCAAAG 11454
QY 530 YTrp---GluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLe 549
Db 11146 CTGGTACCAAGGCCAAACCAACCACTTAATCT----- 11176
QY 549 uLeuLysAsnGluGluIleLeuCysLeuAlaAspAspLeuAlaThrArgLeuThrGlyVa 569
Db 11177 -----TTAAACACAGCAGTACCACCAAC 11199
QY 569 lYrProAlaThrAspAsnPheAlaAlaValSerAlaPheAlaAlaAsn---MetLe 588
Db 11200 ATATACACAACT-----TTTGATGCGCAATGACGACT 11232
QY 588 uSerSerValLeuLysSerGlu-----AlaThrSerSerIleIleLysSerValGl 605
Db 11233 GACGGCGATTTTAAAGAAAGATGCCCAACCAAGCAAGTGCCTTTAAGCGGCAGCTACGC 11292
QY 605 yGluThrAla-ValGlyAlaAlaGlnSer--GlyLeuAlaLysLeuPro 620
Db 11293 TGAACCCGTGACTACGCGCGCAATGTCACCTGCGCGCCACCAATTACCA 11342
RESULT 3
US-09-821-616-33
# Sequence 33, Application US/09821616
# Publication No. US200300271290A1
# GENERAL INFORMATION:
# APPLICANT: Nielsen, Bjarne R.
# APPLICANT: Nielsen, Ruby
# APPLICANT: Lehmbeck, Jan
# TITLE OF INVENTION: Thermostable Glucoamylase
# FILE REFERENCE: 5279.200-US
# CURRENT APPLICATION NUMBER: US/09/821.616
# PRIOR FILING DATE: 2001-03-29
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/199,290
# PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
# PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
# PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
# PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
# PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
# PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-26
# PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
# PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
# NUMBER OF SEQ ID NOS: 34
# SOFTWARE: FastSeq for Windows Version 3.0

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1  PRIOR APPLICATION NUMBER: 60/253,625
2  PRIOR FILING DATE: 2000-11-27
3  PRIOR APPLICATION NUMBER: 60/257,931
4  PRIOR FILING DATE: 2000-12-22
5  PRIOR APPLICATION NUMBER: 60/269,308
6  PRIOR FILING DATE: 2001-02-16
7  NUMBER OF SEQ ID NOS: 14110
8  SOFTWARE: FastSeq for Windows Version 4.0
9  SEQ ID NO 8615
10 LENGTH: 7035
11 TYPE: DNA
12 ORGANISM: Staphylococcus aureus
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: (1)...(7035)
16 US-09-815-242-8615

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Pred. No.:	0.0274	Length:	7038
Score:	124.50	Matches:	146
Percent Similarity:	31.31%	Conservative:	81
Best Local Similarity:	20.14%	Mismatches:	298
Query Match:	3.69%	Indels:	201
DB:	10	Gaps:	29

US-09-677-653A-50 (1-647) x US-09-815-242-8615 (1-7035)

Oy	22	ValSerAlaSerThrValIThrValAsnGlyArgArgAsnGlnArgArgThrGlyArg	41
Db	760	TTAACTGCTAAATACAAATACAGTTAAATAAGATAACTTAAACAAATATATGCAACTTCA	819
Oy	42	GlnValSerProAspAsnPheThrAlaIaIa-----AlaGlnAspLeuAlaGln	58
Db	820	GGTAAATGCCTATATGACCAAAAGTACAGGGGTGCTAAAGCTTAAAGCAATATACAAACAGC	879
Oy	59	SerLeuAspAlaSerThrValIThrPheProAlaAsnIleSerSerMetProClnPheArg	78
Db	880	CAAAAAGCTGCC-----ATTACATTAGGAACACGATTTGACTTAATTAAGAGTTTTCAT	933
Oy	79	AsnTrpAlaLeuSgIyLysIleAspLeuAspSer-----	89
Db	934	-----TTTCTGTGMAAAAGTAATTTTAGTAACAAATATGMAAGCGATGGAATGTGTGA	987
Oy	90	AspSerIleGlyTrpIyPheLys-----	97
Db	988	GATGGTATCGGGTTTGCCCTTTCCACCAGGTATATAGTGAAACAGGGTTAAACGGTGCC	1047
Oy	98	-----TyrLeuAsp	100
Db	1048	GCACTAGCTATTTGGTGGCTTAAGTAACGCAATTTGGCTTCAAAATTAGATACGATACAAAT	1107
Oy	101	ProAlaGlyAlaThrGlnSerAlaArgAlaValGlyGlySerLysIle-----	117
Db	1108	ACATCTACGGCAATTCATTCACGAAAGCGCAAAAGCTGACCCTCTAATCTTACTGTGTGCA	1167
Oy	117	-----	117
Db	1168	GGTGGCTTTGGTCCCTTTGTAAACAAACAGATAGTATGTGTGCATCAACATATACATCA	1227
Oy	118	-----ProAspGlyLeuValLysPheSerVal-----	126
Db	1228	AGTTCAACAGCTATATATGCTGCAAAAGTTAAATGGTTCAACCTACAAACACAGCTTCCAA	1287
Oy	127	AspAlaGlyIleLeuArgGluIleTyrArgnGlnGlyCysProValIThrAspValSerVal	146
Db	1288	GATTTCGATTTTAAT-----TATATGGGTGATACAAAAGTTATGAC-----GTT	1333
Oy	147	ProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPheProMetPheArgThrAla	166
Db	1333	AAATATGACAGGTCAAAACATGACACTATATTT-----TCAGAT	1371
Oy	167	TyrValAlaValAlaSerValGlnAsnLysGlnMetSerLeuAspValValAsnAspLeu	186

Db	1372	TGGATTGGGAAAAGGAGGTACGACCAACTTTTTCATTATCAAT--GACAGCCTCAAC-----	1422
Qy	187	ILIGLITPLLEAsnAsnLeuAlaAspTrpArgTyrValValAspSerGluIntTrpIle	206
Db	1425	-----AGGTGGCGCG-----GAC	1436
Qy	207	AsnPheThrAsnAspThrThrTyrTyrValArgIle---ArgValLeuArpProThrTyr	225
Db	1437	AAATTTCACAAAGTACATATTGGAACTTCGAATATACGAATTCGCTGTACCAAGT	1496
Qy	226	AspVal--ProAspProThrGluGluLeuValArgThrValSerAspTyrArgLeuThrTy	245
Db	1497	GAGATACCTTGATATGACCAACAGCT-----	1522
Qy	245	rLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGluGlyPheTrpIleG	265
Db	1522	-AAAGATTTATTTTCCCCCAAAACATTTCTGGAAATGTGTATCAAGTGTACATATGA	1580
Qy	265	yGlyGlnTyr---AlaLeuThrProThrSerLeuProGluIntYrAspValSerGluAlaTy	284
Db	1581	TAATTAACAATCTCATATGACTGCTTAAGATTTAACTACACATCTGTGTGATAGTTCA	1640
Qy	284	rAlaLeu-----HisTrpLeuThrPheAlaArgProSerSerAlaAl	298
Db	1641	TGCATCAACTTATATATGATATCAATATAAAGCTGTAAATAAGACGAATGCTGCACATCGT	1700
Qy	298	aAlaLeuAlaPheValTrpAlaGlyLeuProGluGlyGlyThrAlaProAlaGlyThrPr	318
Db	1701	GACATATTATTTTCTCATGTATGAAGACACCA-----ACTGTAACTGTAGCAATCA	1751
Qy	318	oAlaTrpGluGlnAlaSerSerGlyGly---TyrLeuThrTrpArgHisArgGlyTh	336
Db	1732	AACCATTTAAAGTGGTAAACCAATGAATCCTATTGTGTGTACTACACACAGATTAAGTAC	1811
Qy	336	rThrPheProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTy	356
Db	1812	AGGGACTGTGACAAATACAGTTACA---GGATTACCAACGGCATTTAAGT-----TA	1855
Qy	356	rAspProAsnAspGlySer-----	362
Db	1860	TGATTTGTCACAGATTAATCATCTGGAGCACCCACCAAAATTTGTCATCAACAGTAC	1919
Qy	363	-----TrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVa	380
Db	1920	AGTAGTATCTACTACCAACAGAAATTAACAATGCAGACACTTTTCAATTAATGTTGT	1979
Qy	380	lAspGluValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVa	400
Db	1980	GGATACGCAGACACCAACACAGTACGCCCAATAGAGATTAATCATCTCAGAAAGTTTTC	2039
Qy	400	lArgValPro-----ProSerAsnAlaTyrThrAsnThrVa	412
Db	2040	AATATCACCGCATTAATATGCTACGCAGACATATAGTGTAATTCAGCAATTAACATACAGT	2099
Qy	412	lPheArgAsnThrLeuGluGluThrArgProSerSerArgValGluGluLeuProMetPr	432
Db	2100	C-----ACAGATTCGCCGCTGTGATTAAACATTCGAT-----	2130
Qy	432	oProAlaAspPheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuTy	452
Db	2131	-----AGCACAATATATCTATTATGTGTACACCA-----	2160
Qy	452	sGluThrLeuGlyCysTyrLeuValHisSerLeuMetArgAsnProValPheGlnLeuTh	472
Db	2161	-----ACAAACATTTGTTACAACTACATTTACATATCGT	2192
Qy	472	rProAlaSerSerPheGlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAs	492
Db	2193	TTTTCACAGATGCGCGATGTAAACAAACGACACCAACTTTTAATATGTGAAGTAAACA	2252
Qy	492	p---LeuProAspTyrThrThrGlyThrArgAspSerPheAspGlnAsnMetSerTh-----	509
Db	2253	TAGCATAGTATTCCTATCAACATCGGAGAGTATCCCAACATATCAACAAAGTGTGTCAAC	2312





OY 364 -----ThAspPheAlaSerAlaGlyAspThrVal 373  
Db 66139 GAAAAATGCACTGTCAGATCTTCAAGTCATGACCTGGCCGAA---GGTGTCCGTAC 66195  
OY 374 ThrPheArgGlnValAlaValAspGlu----- 382  
Db 66196 TATTTCCGTGTTCTGCAGTAATAATGATGTTGGTGAGCCCATGAAATGCCAGAA 66255  
OY 383 ---ValValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrValArg 401  
Db 66256 CCAATTGTAGCCACGACAGACGCTGCT----- 66282  
OY 402 ValProPheSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuGluThrArg 421  
Db 66316 AATTCCTCGCAGCTTACCTTGGCTTAAACCTGACACGATGAGGACCCGCGATCACT 66375  
OY 441 -----AlaAsnAsnPro 444  
Db 66376 GGCTACCTGCTGTAATGAGACAAAGGATCTGACCTGGCTTGAAGCTGTCACACC 66435  
OY 445 Lys-----IleGluGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuVal 460  
Db 66436 AAACAGCTAACTTTCACAGTAGAGCGCTGTGTGAGAAACTGAA-----TATGATTC 66489  
OY 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerPheGlyAlaVal 480  
Db 66490 CGTGTGAGGCGCAAGATATGCTGTGCTATGTAACCCAGACACCTTCTCTCTGTC 66549  
OY 481 SerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAspTyrThrGlyIle 499  
Db 66550 ATCATTAAGAGAGCTCAAAATCGAGCCCACTGCTGACCTC-----ACTGGAAT 66597  
RESULT 6  
US-10-025-380-1055  
; Sequence 1055, Application US/10025380  
; Publication No. US20020182191A1  
GENERAL INFORMATION:  
; APPLICANT: Xu, Jianshun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Smith, Carole L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Clapper, Jonathan D.  
; APPLICANT: Skeiky, Gary R.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Veddyk Thomas S.  
; APPLICANT: Carter, Darlick  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
FILE REFERENCE: 210121.471C14  
CURRENT APPLICATION NUMBER: US/10/025.380  
NUMBER OF SEQ ID NOS: 1129  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1055  
LENGTH: 2872  
TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-025-380-1055  
Alignment Scores: 0.0415 Length: 2872  
Pred. No.: 1

Score: 117.00  
Percent Similarity: 33.26%  
Best Local Similarity: 20.87%  
Query Match: 3.47%  
DB: 9  
Matches: 91  
Conservative: 54  
Mismatch: 170  
Indels: 121  
Gaps: 17  
US-09-677-653a-50 (1-647) x US-10-025-380-1055 (1-2872)  
OY 184 AsnAspLeuIleGluThrPheAsnLeuAlaAspThrArg---TyrValValAspSer 202  
Db 1677 AACACCTCATCTGCCACCTCCACCACTCAGTGTGAGATTCACCACTCAGCAT 1736  
OY 203 GluGlnThrPheAsnPheThrAsnAspThrThrTyrThrValArgIleArgValLeuArg 222  
Db 1737 CAGTCCAGGCTCACTGAATATACAGGTTACTCG----- 1772  
OY 223 ProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAspTyrArg 242  
Db 1773 ---CAGTACCAACAACACAGGCTCAGTAGGATCTACACCTTCTACAGACGCCAG 1829  
OY 243 LeuThr----- 244  
Db 1830 ATCAACCAACCAACTCTCACTGCGACATGACACAGCTAGCGCTGAGTAATC 1889  
OY 245 -----TyrLysAlaIleThrCysGlu-AlaAs 253  
Db 1890 CACCACCTCCCGTAGCAACACAGGTTCTACTCACTCACTCACTGTCACCTGCCACAC 1949  
OY 253 nMetProThrLeuValAspGlnGlyPheThrPheGlyGlyGlnThrAlaLeuThrPro-- 272  
Db 1950 CAGCGAGGCTCAGTAGAGATCTACACCGTC-----TACAGACGAGGCCAG 2000  
OY 273 -----ThrSerLeuProGlnIleThrAspValSerGluAlaTyrAlaLeuHisThr 288  
Db 2001 CTCACCTGAACACAGTGTCTCCCTGCGACACCAACCTCAGTTCGTGTAAGACC 2060  
OY 288 rLeuThrPhe---AlaArgProSerSerAlaAlaAlaAlaAlaPhe-----Va 303  
Db 2061 TACACCTTCACACAGCGGCGGACCTCACTCACTCACTCACTGAGAGACGAC 2120  
OY 303 lTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGluAla 323  
Db 2121 CACCTCGGCGCTCAGTAAGATCTACAGCTTCCCGGACGCGCCTCCACCCAAAC 2180  
OY 323 aserSerGlyGlyTyrLeuThrTrpArgHisGlnGly-----ThrPheProAl 340  
Db 2181 AGGTTACCTGCGACACTCAACACCGACACCTCGGTGAGATCACTACTTCTCCAG 2240  
OY 340 aGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsnAs 360  
Db 2241 CAGCTCA----- 2247  
OY 360 pGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVal 380  
Db 2248 -----GGCTCACTGGAACACACACCTCACTGCGCGCTCCACAC 2288  
OY 380 lAspGluValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrVal 400  
Db 2289 CTCTGCGCTGTTGGAGATTCACACCTCAGCGCTCAGTCAAGTCAACGAAACAC 2348  
OY 400 lArgValProPheSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuGluThr 420  
Db 2349 AACTTACCGGCGAGTCCACAACACCAAGCTCAGTGAATCAACACCTTCTACAC 2408  
OY 420 rArgProSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal 440  
Db 2409 TAGCCCC-----AGATCAACAGATGCAACACTCTCCTGCA-----ACCAAC 2453  
OY 440 lAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCys----- 457  
Db 2454 AAGCTCAGCGCTCAGCAAGAAATCCAGCATCCACAGTCAACAGGCTCAACGACAC 2513  
OY 458 -----TyrLeuValHis 461



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Db 2514 AACAGGTTCCCTGACAGCAGCAGCAACCTCAGGCTCAGTCAGAGAACCTTAAACTTCCCA 11
QY 461 sSerLysMetArgAsnProValPheGlnLeuThrPro-----AlaSerSerph 477
Db 2574 CACGACGCAAGGCTCAACAGAGGCAACACCTGCTCCCTGGCAGTACACAGCAGCTCATCTCCCT 2633
QY 477 eGlyAlaValSer-----PheAsnAsnProGlyTyrGlnArgThrArgAspLeuPr 494
Db 2634 TGGTCAACAATCTACAACTCTTCCACAGCAGCAGCCGAGGAGACATGTAAACACACTCTTACC 2693
QY 494 oAspTyrThr-----GlyIleArgAsp-----SerPheAspG1 505
Db 2694 TGAATGACACCATTAACCTCAGGCTCGTGAGGAGATCTACACCCACCCAGCAGCAGCTGG 2753
QY 505 nasMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerCysSerIleValTh 525
Db 2754 CTGCTACACACAACTGACCCCTGCGCAGCTCCACAAAGCGCTGGCTTCAGGAAGAATC 2813
QY 525 rLysThrTyrGlnGlyTyrPheGlnGlyValThrAsnValAsnThrPro 540.
Db 2814 TACTACTTCTCCAGAGCTGGCCAGCTCAAGTGAC--ACAACACCT 2856

RESULT 7
US-09-922-217-1055
; Sequence 1055, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1055
; LENGTH: 2872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1055

Alignment Scores:
Pred. No.: 0.0415 Length: 2872
Score: 117.00 Matches: 91
Percent Similarity: 33.26% Conservative: 54
Best Local Similarity: 20.87% Mismatches: 170
Query Match: 3.47% Indels: 121
DB: 10 Gaps: 17

US-09-677-653a-50 (1-647) x US-09-922-217-1055 (1-2872)

QY 184 AsnAspLeuIleGluTyrPheAsnAsnLeuAlaAspTyrArg--TyrValValAspSer 202
Db 1677 AACAGCCTCATCTGCCCCACATCCACAACTCAGTGTGAGAAATCTACAACTCAGCAT 1736
QY 203 GlnGlnTyrPheAsnPheThrAsnAspThrTyrTyrValArgIleArgValLeuArg 222
Db 1737 CAGTCCAGGCTCACTGAATAATACAAACGTTACTGG----- 1772
QY 223 ProThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAspTyrArg 242
Db 223 ProThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAspTyrArg 242

Db 1773 ---CAGTACACAACAACAGGCGCTCAGTGAAGCATCTACACCTTCTACAGCAGCCAG 1829
QY 243 LeuThr----- 244
Db 1830 ATCACCACCAACAACACTCTACCTCGCAGCAGACAGAGCTAGGCGTGGTGAAGATC 1889
QY 245 -----TyrLysAlaIleThrCysGln-AlaAs 253
Db 1890 CACCACCTCCCGTAGCCACACAGGTTTACTACTACACAGTGTACTCTGCAGCAGCAG 1949
QY 253 nMetProThrLeuValAspGlnGlyPheThrPheGlyGlyGlnTyrAlaLeuThrPro-- 272
Db 1950 CAGCGCAGGCTCAGTAGGAATCTACACCGTC-----TACAGCAGCAGCCAGG 2000
QY 273 -----ThrSerLeuProGlnTyrAspValSerGlnAlaTyrAlaLeuHisTh 288
Db 2001 CTCAACTGAACAACACACTGTCTCCCTGCACACACACACACTCAGTTGCTGTGAAGGCC 2060
QY 288 rLeuThrPhe---AlaArgProSerSerAlaAlaAlaLeuAlaPhe-----Va 303
Db 2061 TACACCTTCCACAGCGCGCCAGCTTACTACACACACACTGTTCCTAGGACAGCAG 2120
QY 303 lTyrPheGlyLeuProGlnGlyGlyThrAlaProAlaGlyTyrProAlaTyrPheGlnAl 323
Db 2121 CACCTCGGCGCTCAGTAGAATCTCAGACCTTCCCGGAGCGCAGCAGCTCCACCCAAAC 2180
QY 323 aSerSerGlyGlyTyrIleuThrThrPheArgHisAsnGly-----ThrThrPheProAl 340
Db 2181 AGGGTTACCTGCCACACTCACAACCCGAGCCTCGGAGAGAAATCAACTCTCTTCCAG 2240
QY 340 aGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGlnValArgTyrAspProAsnAs 360
Db 2241 CAGCTCA----- 2247
QY 360 pGlySerTyrThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVa 380
Db 2248 -----GGCTCACTGMAACAACACTCCTCAGCTCCGCTCAGCAGC 2288
QY 380 lAspGlnValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVa 400
Db 2289 CTGCGCCTGGTGGAGAAATCCACACCTCAGCTCAGTCCAGTCAACGCAACGAAAC 2348
QY 400 lArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGlnTh 420
Db 2349 AACTTACCCGGCAGTCCACACACACAGCCTCAGTGAAGAAATCAACACCTTCTACAC 2408
QY 420 rArgProSerSerArgArgIleGlnGlnLeuProMetProProAlaAspPheGlyGlnThVa 440
Db 2409 TAGCCCC-----AGATCACCAAGATGCACACTCTCAGCTGCA-----ACCACAAAC 2453
QY 440 lAlaAsnAsnProLysIleGlnGlnSerLeuLeuGlnThrLeuGlnCys----- 457
Db 2454 AAGCTCAGGCGTCAGCGAAGAAATCCACATCCACAGTCAACAGGCTCAACGACAC 2513
QY 458 -----TyrLeuValH1 461
Db 2514 AACAGCCTTCCCTGACAGCAGCAGCAGCAGCTCAGGCTCAGTCAGAGAACCTTAAACTTCCCA 2573
QY 461 sSerLysMetArgAsnProValPheGlnLeuThrPro-----AlaSerSerph 477
Db 2574 CACGACGCAAGGCTCAACAGAGGCAACACCTGCTCCCTGGCAGTACACAGCAGCTCATCTCCCT 2633
QY 477 eGlyAlaValSer-----PheAsnAsnProGlyTyrGlnArgThrArgAspLeuPr 494
Db 2634 TGGTCAACAATCTACAACTCTTCCACAGCAGCAGCCGAGGAGACATGTAAACACACTCTTACC 2693
QY 494 oAspTyrThr-----GlyIleArgAsp-----SerPheAspG1 505
Db 2694 TGAATGACACCATTAACCTCAGGCTCGTGAGGAGATCTACACCCACCCAGCAGCAGCTGG 2753
QY 505 nasMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerCysSerIleValTh 525
Db 2754 CTGCTACACACAACTGACCCCTGCGCAGCTCCACAAAGCGCTGGCTTCAGGAAGAATC 2813

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Qy 525 rlysthrTYrGlnGlyTrpGlnGlyValThrAsnValAsnThrPro 540  
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 Db 2814 TACTACTTTCAGAGCTGGCCAGCTCAAGTGAC---ACAACACCT 2856

## RESULT 8

US-09-833-263-1055  
 ; Sequence 1055, Application US/09833263  
 ; Patent No. US20020110547A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, Aijun  
 ; APPLICANT: Clapper, Jonathan D.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Meagher, Madeline J.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE  
 ; FILE REFERENCE: 210121.471C12  
 ; CURRENT APPLICATION NUMBER: US/09/833,263  
 ; NUMBER OF SEQ ID NOS: 1093  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 1055  
 ; LENGTH: 2872  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-833-263-1055

## Alignment Scores:

Pred. No.:	0.0415	Length:	2872
Score:	117.00	Matches:	91
Percent Similarity:	33.26%	Conservative:	54
Best Local Similarity:	20.87%	Mismatches:	170
Query Match:	3.47%	Indels:	121
DB:	10	Gaps:	17

US-09-677-653a-50 (1-647) x US-09-833-263-1055 (1-2872)

Qy 184 AsnAspLeuIleGlnTrpLeuAsnLeuAlaAspTrpArg---TyrValAlaAspSer 202  
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 Db 1677 AACACCTTCATCTGCCATCCACAACCTCAGCTCGTGAATCTCAACCTCAGCAT 1736  
 Qy 203 GlnGlnTrpIleAsnPheThrAsnAspThrTrpTrpValArgIleArgValLeuArg 222  
 : ||||| ||||| : ||||| |||||  
 Db 1737 CAGTCCAGGCTCACTGAAATTAACAAGCTTACCTGG----- 1772  
 Qy 223 ProThrTrpAspValProAspProThrGlnGlyLeuValArgThrValSerAspTrpArg 242  
 : ||||| ||||| : ||||| |||||  
 Db 1773 ---CAGTACACACACACAGGCTCAGTAGGACATCTACACCTCTACAGAGCCCCAG 1829  
 Qy 243 LeuThr----- 244  
 : ||||| ||||| : ||||| |||||  
 Db 1830 ATCACCACACACACAGCTCTCAGCTGACATGACAGCTAGGCGTGTGAAGAAATC 1889  
 Qy 245 -----TyrLysAlaIleThrCysGluAlaAs 253  
 : ||||| ||||| : ||||| |||||  
 Db 1890 CACCACTTCCTAGCCAAACAGGTTTACTACTACACAGTGTACCTGCCAGCAGCACAC 1949  
 Qy 253 mMetProThrLeuValAspGlnGlyPheThrPheGlnGlyGlnTrpAlaLeuThrPro-- 272  
 : ||||| ||||| : ||||| |||||  
 Db 1950 CACGCGACAGGCTCAGTGAATCTACACCTG-----TACAGCAGCAGCCAGG 2000  
 Qy 273 -----ThrSerLeuProGlnTrpAspValSerGluAlaTyrAlaLeuHisTh 288  
 : ||||| ||||| : ||||| |||||  
 Db 2001 CTCAACTGAACACACAGTTCCTCGCAGACACCAACCTCAGTTCGTGTGAAGAGCC 2060  
 Qy 288 rLeuThrPhe---AlaArgProSerSerAlaAlaAlaAlaAlaPhe-----Va 303  
 : ||||| ||||| : ||||| |||||  
 Db 2061 TACAACCTTTCACACCGCGCAGCTCACTCACTCAACACACTGTCTACTGAGAGACGAC 2120  
 Qy 303 lTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlnGlyThrProAlaTrpGlnGlnAl 323  
 : ||||| ||||| : ||||| |||||  
 Db 2121 CACCTCGGGCTCTACTGAAGAAATCTACAGCCTTCCCGGAGCCAGCCTCCACCCAAAC 2180

Qy 323 aSerSerGlyGlyTyrLeuThrTrpArgHisAsnGly-----ThrThrPheProAl 340  
 : ||||| ||||| : ||||| |||||  
 Db 2181 AGGTTACCTGCCACACCTACACACCCAGACCTCGGTGAGAACTCAACTACTTCCAG 2240  
 Qy 340 aGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGlnArgTyrAspProAsn 360  
 : ||||| ||||| : ||||| |||||  
 Db 2241 CAGCTCA----- 2247  
 Qy 360 pGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVa 380  
 : ||||| ||||| : ||||| |||||  
 Db 2248 -----GGCTCACTGGAAACACACACTCTACCTGCCCGCTCCACAC 2288  
 Qy 380 lAspGlnValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrVa 400  
 : ||||| ||||| : ||||| |||||  
 Db 2289 CTCTGGCTCTGTGGAAATCCACACCTCAGCCCTCAGTCCAGCTCAACGAAACAAAC 2348  
 Qy 400 lArgValProProSerAsnAlaTyrThrAsnThrValPheArgAspThrLeuLeuLuh 420  
 : ||||| ||||| : ||||| |||||  
 Db 2349 AACTTACCCGGCAGTCCACACACACACAGCTCAGTGAAGAAATCAACCTTCTACAC 2408  
 Qy 420 rArgProSerSerArgArgLeuGlnLeuProMetProProAlaAspPheGlyGlnThrVa 440  
 : ||||| ||||| : ||||| |||||  
 Db 2409 TAGCCCC-----AGATCACAGAGATGCAACACTCTACCTGCA-----ACGCACAC 2453  
 Qy 440 lAlaAsnAsnProLysIleGlnIleSerLeuLeuLysGlnThrLeuGlyCys----- 457  
 : ||||| ||||| : ||||| |||||  
 Db 2454 AAGCTCAGCGTCAGCGAAGAAATCCAGCACATCCACAGTCAACAGCTCAACGACACAC 2513  
 Qy 458 -----TyrLeuValHis 461  
 Db 2514 AACAGCTTCCTCGACAGACACACACCTCAGGCTCAGTCAAGAACTTAAACTTCCCA 2573  
 Qy 461 sSerIleMetArgAsnProValPheGlnLeuThrPro-----AlaSerSerPh 477  
 : ||||| ||||| : ||||| |||||  
 Db 2574 CAGCAGCCCAAGGCTCAGAGAGGACACACTGTCCTCGGACAGACACAGCCTCATCCCT 2633  
 Qy 477 eGlyAlaValSer-----PheAsnAsnProGlyTyrGluArgThrArgAspLeuR 494  
 : ||||| ||||| : ||||| |||||  
 Db 2634 TGGTCAACATCTACACCTTCACAGCGCCAGCGACACTGAAACCACTCTTAC 2693  
 Qy 494 oAspTyrThr-----GlyIleArgAsp-----SerPheAsp 505  
 : ||||| ||||| : ||||| |||||  
 Db 2694 TGAATACACATTAACCTCAGGCTCTCGTAGGACATCTACACCCACACAGACAGCTGG 2753  
 Qy 505 nasMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerCysSerIleValTh 525  
 : ||||| ||||| : ||||| |||||  
 Db 2754 CTGCTACACACACACAGCTGACCCCTCGCAGCTCCACAAAGCGCTGGCTTCAGAGAATC 2813  
 Qy 525 rlysthrTYrGlnGlyTrpGlnGlyValThrAsnValAsnThrPro 540  
 : ||||| ||||| : ||||| |||||  
 Db 2814 TACTACTTTCAGAGCTGGCCAAAGCTCAAGTGAC---ACAACACCT 2856

## RESULT 9

US-09-554-000-1  
 ; Sequence 1, Application US/09554000  
 ; Patent No. US20020165364A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tsien, Roger Y.  
 ; APPLICANT: Miyawaki, Atsushi  
 ; TITLE OF INVENTION: DETECTION OF ANALYTES  
 ; FILE REFERENCE: 07257/042001  
 ; CURRENT APPLICATION NUMBER: US/09/554,000  
 ; CURRENT FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: 08/818,252  
 ; PRIOR FILING DATE: 1997-03-14  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1929  
 ; TYPE: DNA  
 ; ORGANISM: Aequorea victoria  
 ; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (0)...(1926)
US-09-554-000-1

Alignment Scores:
Pred. No.: 0.0255 Length: 1929
Score: 116.50 Matches: 106
Percent Similarity: 36.46% Conservative: 61
Best Local Similarity: 23.14% Mismatches: 154
Query Match: 3.45% Indels: 137
DB: 9 Gaps: 26

US-09-677-653a-50 (1-647) x US-09-554-000-1 (1-1929)

QY 2 GLYAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 GGTCCTCTGAGTTCTGTGACCGCCGCCGATCATGACCACTGACAGAGCA--- 713

QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 714 ---GATTGCAGAGTTCAAGAAGCCTTCATTTTCGACAGAGATGGGACGACCAT 770

QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProAspAsn 49
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 771 CACCACAAAGAACTTGGCACCCGTTATGAGTCCGCTTGACCAAAACCAAGCAA--- 825

QY 49 eThrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThrValTh 66
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 826 ---GCAGAAATTCAGAGATATGATCAATGAAGTGCATGCGCATGCAATGCAAGATT 881

QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnThrPalAlaGlySileAs 86
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 882 CTTTCCGCAATTTCTTACTATGATG-----CCTGAAAAATGAAGA 923

QY 86 pleuAspSer---AspSerIleGlyThrPyrPheLeuSyrLeuAspProAlaGly---- 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 924 CACAGACAGCGAAGAAATCCGAGAAGATCCGTTTGTGACAAGATGGGAACGG 983

QY 104 -----AlaThrIleSerAlaAlaArgAlaValGlyGluTyrSerIleProAspG 120
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 984 CTACATCAGCGCTGCTCAATTAATACGTCACGTCATG-----ACAAACCTCGGGAGAA 1034

QY 120 yLeuValIlyPheSerValAspAlaGluIleArgGluIle----- 133
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1035 GTTAACGATGAGAAAGTGTGATGATGATGAAGGAAAGCAATATTCATGCTGATGCCA 1094

QY 134 -----TyrAsnGluGluCysProValValThrAspValSerValProLeuAspG 151
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1095 AGTAACACTATGAGAGTTTGTACAAATGATGACAGCAAGGGG-----GGGAAGAG 1145

QY 151 gGlnTrpSerLeuSerIlePheSerPheProMetPheArgThrAlaTyrValAlaValAl 171
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1146 GCCTGTGAAGAAAACCTTCATTTGCC-----GTCAACGCTGC 1181

QY 171 aasn-----ValGluAsnIlySgluMetSerLeuAs 181
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1182 CAACCGGTTCAAGAAATCTCCAGCTCATGCTGAGCAAGGCGAGGAGCTTCCACCGG 1241

QY 181 pValValAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAs 201
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1242 GGTGTGCTCCATCCTGTGTGAGCGGAGCGGCAAGTAAAGGCGCAAGTTACACGTGC 1301

QY 201 pSerGluGlnTrpIleAsnPheThrAsnAspThrThrTyr---TyrValArgIleArgVa 220
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1302 CGCGGAGGCG-----GAGGGCGATGCCACCTACGCGCAAGCTGACCCCTGAAGTT 1349

QY 220 lLeuArgProThrTyrAspValProAspProThrGluGluValLeuValArgThrValSerAs 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1350 CATGTGACCAACGCGAGCTGCCGCTGCGCCGACCACTGCTGACCAAC----- 1401

QY 240 pTyrArgLeuThrTyrIlyAlaIleThrCysGluAlaAsnMetProThrIleuValAspG 260
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1402 -----CTGACCTAC-----GGCGTGAGTGCTTTCAGCGCGTACCCGACCAACATGAAG-- 1449

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QY 260 nGlyPheTrpIleGlyGlnTyrAlaLeuThrProThrSerLeuProGluIlyAspVa 280
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1450 -----CAGCAGACCTTCTCAAGTCCGCGCAATGCCAAGGCTACGT 1490

QY 280 lSerGluAlaTyrAlaLeuHisThrLeuThrPheAlaArg-ProSerSerAlaAlaAl 300
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1491 CCAGAGAG-----CGCACCATCTTCTTCAAGAGCA 1520

QY 300 euAlaPheValTrpAlaGlyLeuProGluGlyThrAlaProAla----- 315
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1521 CGGCA-----ACTACAGACCCCGCCGCGAGTGAAGTT 1553

QY 316 -----GlyThrProAlaTrpGluGlnAlaSerSerGlyTyrLeuThrTrpArgHis 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1554 CGAGGGCGACACCC---TGGGAACCCATCAGCTTAAGGCGCATGCACTTCAAGAGCA 1610

QY 334 snGlyThrThrPheProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuG 354
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1611 CGGCACATCTCTGGGCGACA----- 1630

QY 354 luarGlyAspProAsnAspIlySerTrpThrAspPheAlaSerAlaGlyAspThrVal- 373
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1631 -----AGCTGAGTACAACTACACACAGCCACCAACGTCTATAT 1667

QY 374 -----ThrPheArgGlnValAlaVal-----AspGluValValThrAsnAsp 389
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1668 CATGGCCGACAGCAAGCAAGGCAATCAAGTGAAGTCAAGTTCAGATCCGCCACAACTCA 1727

QY 389 roAlaGlyGlyGlySerAlaProThrPheThrValArgValProProSer 405
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1728 GGAGGCGACGCTGCAGCTCGCCGACACTACACAGCAACCCCATCG 1777

RESULT 10
US-09-554-000-5
; Sequence 5, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Acsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Aequorea victoria.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1926)
US-09-554-000-5

Alignment Scores:
Pred. No.: 0.0255 Length: 1929
Score: 116.50 Matches: 105
Percent Similarity: 36.70% Conservative: 62
Best Local Similarity: 23.08% Mismatches: 157
Query Match: 3.45% Indels: 131
DB: 9 Gaps: 25

US-09-677-653a-50 (1-647) x US-09-554-000-5 (1-1929)

QY 2 GLYAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 GGTCCTCTGAGTTCTGTGACCGCCGCCGATCATGACCACTGACAGAGCA--- 713

QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 714 ---GATTGCAGAGTTCAAGAAGCCTTCATTTTCGACAGAGATGGGACGACCAT 770

QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProAspAsn 49
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 771 CACCACAAAGAACTTGGCACCCGTTATGAGTCCGCTTGACCAAAACCAAGCAA--- 825

QY 49 eThrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThrValTh 66
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 826 ---GCAGAAATTCAGAGATATGATCAATGAAGTGCATGCGCATGCAATGCAAGATT 881

QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnThrPalAlaGlySileAs 86
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 882 CTTTCCGCAATTTCTTACTATGATG-----CCTGAAAAATGAAGA 923

QY 86 pleuAspSer---AspSerIleGlyThrPyrPheLeuSyrLeuAspProAlaGly---- 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 924 CACAGACAGCGAAGAAATCCGAGAAGATCCGTTTGTGACAAGATGGGAACGG 983

QY 104 -----AlaThrIleSerAlaAlaArgAlaValGlyGluTyrSerIleProAspG 120
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 984 CTACATCAGCGCTGCTCAATTAATACGTCACGTCATG-----ACAAACCTCGGGAGAA 1034

QY 120 yLeuValIlyPheSerValAspAlaGluIleArgGluIle----- 133
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1035 GTTAACGATGAGAAAGTGTGATGATGATGAAGGAAAGCAATATTCATGCTGATGCCA 1094

QY 134 -----TyrAsnGluGluCysProValValThrAspValSerValProLeuAspG 151
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1095 AGTAACACTATGAGAGTTTGTACAAATGATGACAGCAAGGGG-----GGGAAGAG 1145

QY 151 gGlnTrpSerLeuSerIlePheSerPheProMetPheArgThrAlaTyrValAlaValAl 171
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1146 GCCTGTGAAGAAAACCTTCATTTGCC-----GTCAACGCTGC 1181

QY 171 aasn-----ValGluAsnIlySgluMetSerLeuAs 181
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1182 CAACCGGTTCAAGAAATCTCCAGCTCATGCTGAGCAAGGCGAGGAGCTTCCACCGG 1241

QY 181 pValValAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAs 201
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1242 GGTGTGCTCCATCCTGTGTGAGCGGAGCGGCAAGTAAAGGCGCAAGTTACACGTGC 1301

QY 201 pSerGluGlnTrpIleAsnPheThrAsnAspThrThrTyr---TyrValArgIleArgVa 220
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1302 CGCGGAGGCG-----GAGGGCGATGCCACCTACGCGCAAGCTGACCCCTGAAGTT 1349

QY 220 lLeuArgProThrTyrAspValProAspProThrGluGluValLeuValArgThrValSerAs 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1350 CATGTGACCAACGCGAGCTGCCGCTGCGCCGACCACTGCTGACCAAC----- 1401

QY 240 pTyrArgLeuThrTyrIlyAlaIleThrCysGluAlaAsnMetProThrIleuValAspG 260
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1402 -----CTGACCTAC-----GGCGTGAGTGCTTTCAGCGCGTACCCGACCAACATGAAG-- 1449

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Db 714 ---GATTGAGAGTCAAGAACCTTCATCATTCACAGATGAGGAGCGCACAT 770
QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProProAspAsnPh 49
Db 771 CACCACAAAGAAAGAACTGGACCGCTTATGAGTCGCTGGACAACCAAGGAA----- 825
QY 49 eThraAlaAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThraValTh 66
Db 826 ---GCAGAAATTCAGAGATATGATCATAGATGATGATGCTGATGCGCATGGAACGATTTA 881
QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnTrpAlaLysGlyLysIleAs 86
Db 882 CTTTCCTGATTTCTTACTATGATG-----GCTAGAAAATGAAAGA 923
QY 86 pleuAspSer---AspSerIleGlyTrpTrpPheLysTrpLeuAspPro-----AlaG 103
Db 924 CACAGACAGCGAAGAAATCCGAGACGATTCCTGTTTGTGACAGAGATGGAAACGG 983
QY 103 yAlaTrpGlnSerAlaArgAlaValGlyLysTrpSerLysIleProAspGlyLeuValLys 123
Db 984 CTACATCAGCGCGCTCAGTTCAGTCAGTCATGACAAACCTCGGGGAGAAAGTTAACGA 1043
QY 123 sPheSerValAspAlaGlnIleArgGluIle-----Tyr 134
Db 1044 TGAAGAAGTTGATGAATGATAGGAGACAGATATCGATGGTATGCCAAGTAAACTTA 1103
QY 134 rAsnGlnGluCysProValAlaThrAspValSerValProLeuAspGlyArgIleTrpSe 154
Db 1104 TGAAGCTTTGTCATCAATGATGACACCAAGGCG-----GGACAGAGGGGCTGGAA 1154
QY 154 rLeuSerIlePheSerPheProMetPheArgTrpAlaTyrValAlaValAlaAsn----- 172
Db 1155 GAAAACTTCATTGCC-----GTGACGGCTGCCAACCGGTT 1190
QY 173 -----ValGluAsnLysGluMetSerLeuAspValValAs 184
Db 1191 CAGAAGATCTCCGACCTCATGCTGAGCAAGGCGAGGCTGTTCCACGGGCTGTGTC 1250
QY 184 nAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTrpValValAspSerGlu 204
Db 1251 CATCCGCTGCTGAGCTGAGCGGACGCTAAAGCGCCACAAAGTTGAGCTGCTCGCGCA 1310
QY 204 nTrpIleAsnPheThrAsnAspThrTrp---TyrValArgIleArgValLeuArgPr 223
Db 1311 C-----GAGCGGATGCCACCTTAAGCGCAAGCTGACCTGAACTTCATCTGCAC 1358
QY 223 oThrTrpAspValProAspProThrGluGluValAlaGlyThValSerAspTrpArgLe 243
Db 1359 CACCGGCAAGCTGCGCTGCTGCGCCACCTCGTGCAGCCAC-----CT 1403
QY 243 uThrTrpLysAlaIleThrCysGluValAsnMetProThrLeuValAspGlnGlyPheTr 263
Db 1404 GACCTAC---GGCGTGCATGCTCTCAGCCGCTAACCCGACACATGAAG----- 1449
QY 263 pIleGlyGlnIlyrAlaLeuThrProThrSerLeuProGlnIlyrAspValSerGluAl 283
Db 1450 -----CAGACAGACTTCTTCAAGTCGCGCATGCCGAAGGCTAGCTCAGAGAG-- 1497
QY 283 eTyrAlaLeuHisThrLeuThrPheAlaArg--ProSerSerAlaAlaAlaLeuAlaPhe 303
Db 1498 -----CGACACATCTTCTTCMAAGAGACGAGCGGCA----- 1525
QY 303 aTrpAlaGlyLeuProGlnGlyGlyThAlaProAla-----GlyT 317
Db 1526 -----ACTACAAAGACCGCGCGGAGGTAAGTTGAGGGCGA 1562
QY 317 hPProAlaTrpGlnAlaAspSerGlyGlyTyrIleuThrTrpArgHisAsnGlyThr 337
Db 1563 CACCC---TGCTGAACCGCATGAGCTGAAGGCAATCGACTTCACAGAGAGCGCAACT 1619
QY 337 hPheProAlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGluAlaGlyTyr 357

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Db 1620 CCTGGGCGACA----- 1630
QY 357 sPProAsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrVal-----T 374
Db 1631 -----ACGTGAGTACACTACACACACGCTCTATATCTATGCGCCA 1676
QY 374 hPheArgGlnValAlaVal-----AspGluValValTrpAsnAspProAlaGly 392
Db 1677 CAAAGCAAGAAAGACGGATCAAGGTGAAGTTCAGAGATCCGCGACACATGAGAGCGG 1736
QY 392 yGlySerAlaProThrPheThrValAlaValProSer 405
Db 1737 CGTGACGCTGCGCGACCTACCGACGAACACCCCATCG 1777

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## RESULT 11

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US-09-554-000-3
; Sequence 3, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1956)
US-09-554-000-3

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## Alignment Scores:

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Pred. No.: 0.0261 Length: 1959
Score: 116.50 Matches: 106
Percent Similarity: 36.46% Conservative: 61
Best Local Similarity: 23.14% Mismatches: 154
Query Match: 3.45% Indels: 137
DB: 9 Gaps: 26

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US-09-677-653a-50 (1-647) x US-09-554-000-3 (1-1959)

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QY 2 GlyAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
Db 657 GGTCCCTGCTGAGATGCTGACGCCGCCGACATGACCAACTGACGAAGAGCA--- 713
QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34
Db 714 ---GATTGAGAGTTCAAGAAAGCCTTCATTCATTCATTCGACAAAGATGAGGAGCGCACAT 770
QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProProAspAsnPh 49
Db 771 CACCACAAAGAAAGAACTGGACCGTTATGAGTCGCTTGGACAACCAACCAAGGAA----- 825
QY 49 eThraAlaAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThraValTh 66
Db 826 ---GCAGAAATTCAGAGATATGATCATAGATGATGATGCTGATGCGCATGGAACGATTTA 881
QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnTrpAlaLysGlyLysIleAs 86
Db 882 CTTTCCTGATTTCTTACTATGATG-----GCTAGAAAATGAAAGA 923
QY 86 pleuAspSer---AspSerIleGlyTrpTrpPheLysTrpLeuAspProAlaGly----- 103
Db 924 CACAGACAGCGAAGAAATCCGAGACGATTCCTGTTTGTGACAGAGATGGAAACGG 983

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QY 104 -----AlaThrGluSerAlaIaArgAlaValGlyGluTyrSerLysIleProAspG1 120
      ||| |||
      ||| |||
Db 984 CTACATCAGCGCTGCTGAATTAAGTCACTCATG-----ACAACCTCGGGGGAA 1034
QY 120 yLeuValLysPheSerValAspAlaGluIleArgGluIle----- 133
      ||| |||
      ||| |||
Db 1035 GTTAAACAGATGAAGAAGTTGATGAATGATAAAGGAAGCAGATATGATGATGCGCA 1094
QY 134 -----TyrAsnGluGluLucyProValIaThrAspValSerValProLeuAspGlyAr 151
      ||| |||
      ||| |||
Db 1095 AGTAAACTATGAAGAGTTGTCTACAAATGATGACACGAAAGGG-----GGGAGAG 1145
QY 151 gGlnTyrPseLeuSerIlePheSerPheProMetPheArgThrAlaTyrAlaValAla 171
      ||| |||
      ||| |||
Db 1146 GCGCTGGAGAAAACTTCTATTC-----GTCAGCGCTGC 1181
QY 171 aasn-----ValGluAsnLysGluMetSerLeuAs 181
      ||| |||
      ||| |||
Db 1182 CAACCGGTTCCAAAGAGATCTCCAGCTCATGTCAGACGAGGCGAGAGCTGTTCACCG 1241
QY 181 pValValAsnAspLeuIleGluTyrLeuAsnAsnLeuAlaAspTyrArgTyrValValAs 201
      ||| |||
      ||| |||
Db 1242 GGTGGGCCCATCTGCTGCTGACGCGACGCGCAAGGCGCACAGTTTCAGCGCTGC 1301
QY 201 pSerGluGlnTyrIleAsnPheThrAsnAspThrThrTyr--TyrValArgIleArgVa 220
      ||| |||
      ||| |||
Db 1302 CGGCGAGGCG-----GAGGCGCATGCCACCTTACGCGAAGCTGACCTGAAGTT 1349
QY 220 IleuArgProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAs 240
      ||| |||
      ||| |||
Db 1350 CATCTGCACACCGGCAAGCTGCCGCTGCCGCCACCTGTCGTCAGCACCC----- 1401
QY 240 pTyrArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspG1 260
      ||| |||
      ||| |||
Db 1402 -----CTGACCTAC--GGCGTGCAGTCTTCAGCCGCTACCCGACCCACCATGAAG-- 1449
QY 260 nGlyPheThrIleGlyGlyGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspVa 280
      ||| |||
      ||| |||
Db 1450 -----CAGCACGACTTCTCAAGTCCGCCATCGCCCAAGGCTACGT 1490
QY 280 IserGluAlaTyrAlaLeuHisThrLeuThrPheAlaArg-ProSerSerAlaAlaAlaL 300
      ||| |||
      ||| |||
Db 1491 CCAGGAG-----CGCACCATCTCTTCTTCAAGGACGA 1520
QY 300 euAlaIheValIrrPalaglyLeuProGlnGlyGlyThrAlaProAla----- 315
      ||| |||
      ||| |||
Db 1521 CGGCA-----ACTACAAAGACCCCGCGCGAGGTGAAGTT 1553
QY 316 -----GlyThrProAlaTyrPgluGlnAlaSerSerGlyGlyTyrLeuThrTyrArgHisA 334
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      ||| |||
Db 1554 CGAGGCGGACACCC--TGGTGAACCGCATCGAGCTGAAGGCGATGACTTCAAGGACGA 1610
QY 334 snGlyThrThrPheProAlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeuG 354
      ||| |||
      ||| |||
Db 1611 CGGCACATCTGGGCACA----- 1630
QY 354 LuuArgTyrAspProAsnAspGlySerTyrPheThrAspPheAlaSerAlaGlyAspThrVal- 373
      ||| |||
      ||| |||
Db 1631 -----AGCTGGAGTACAACTACACACGACCAACGCTATAT 1667
QY 374 -----ThrPheArgGlnValAlaVal-----AspGluValAlaValThrAsnAsp 389
      ||| |||
      ||| |||
Db 1668 CATGGCGGACAAAGCAAGAAAGCGCATCAAGTGAACTTCAAGTCCGCCCAACATCGA 1727
QY 389 roAlaGlyGlySerAlaProThrPheThrValArgValProProSer 405
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      ||| |||
Db 1728 GGAGGCGAGCGTGCAGCTCGCGACCATCTACAGACAAACACCCCATCG 1777
RESULT 12
US-09-554-000-7
; Sequence 7, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
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; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1968)
US-09-554-000-7
Alignment Scores:
Pred. No.: 0.0264 Length: 1971
Score: 116.50 Matches: 105
Percent Similarity: 36.70% Conservative: 62
Best Local Similarity: 23.08% Mismatches: 157
Query Match: 3.45% Indels: 131
DB: Gaps: 25
US-09-677-653a-50 (1-647) x US-09-554-000-7 (1-1971)
QY 2 GlyAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
      ||| |||
      ||| |||
Db 705 GGTCTGCTGAGAGTCTGTGACCCCGCCCGCATGATGACCAACTACAGAAAGCA--- 761
QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34
      ||| |||
      ||| |||
Db 762 ---GATTGCAGAGTTCAAAGAACGCTTCATATTCGACAAAGATGGGAGCGACCAT 818
QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProAspAsnPh 49
      ||| |||
      ||| |||
Db 819 CACCACAAAGAACTGGCCACCGTTAGAGTCTTGGACAAACCAACGAGGA----- 873
QY 49 eThrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThrValTh 66
      ||| |||
      ||| |||
Db 874 ---GCAGATTGCGAGATATGATCAATGAATGATGATGATGATGATGATGATGATGAT 929
QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnTrrPalaglyLysIleAs 86
      ||| |||
      ||| |||
Db 930 CTTTCCGATTTCTTACTATGATG-----GCTAGAAAATGAAGGA 971
QY 86 pleuAspSer---AspSerIleGlyTyrPheLysTyrLeuAspPro-----AlaG1 103
      ||| |||
      ||| |||
Db 972 CACAGACAGCGAAGAGAAATCCGAGAAAGCATTCGCTTTTGGACAAAGATGGGAACGG 1031
QY 103 yAlaThrGluSerAlaArgAlaValGlyGluTyrSerLysIleProAspGlyLeuValLys 123
      ||| |||
      ||| |||
Db 1032 CTACATCAGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1091
QY 123 sPheSerValAspAlaGluIleArgGluIle-----Tyr 134
      ||| |||
      ||| |||
Db 1092 TGAAGAAGTGTGATGAATGATTAAGGAGACAGATATGATGATGATGATGATGATGAT 1151
QY 134 rAsnGluGluLucyProValValThrAspValSerValProLeuAspGlyArgGlnTrrPse 134
      ||| |||
      ||| |||
Db 1152 TGAAGAGTTTGTCAAAATGATGACACCAAGGGG-----GGGAAAGCGCGTGA 1202
QY 154 rLeuSerIlePheSerPheProMetPheArgThrAlaTyrValAlaValAlaAsn----- 172
      ||| |||
      ||| |||
Db 1203 GAAAACTTCTATTC-----ValGluAsnLysGluMetSerLeuAspValValAs 184
QY 173 ----- 1238
Db 1239 CAAGAAGATCTCGAGCTCATGTGTGAGCAAGGCGGAGGAGCTGTTCACCGGGGTGGTGC 1298
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Db 12001 CAAACCTATGTGGCGCGGTGCTGGCGGATGGCACTGGAGCGTCGCC----- 12048  
QY 271 ThrProThrSerLeuProGlnTyrAspValSerGluAlaLeuHisThrLeuThr 290  
Db 12049 -----GTTCCGGCGGTGATGTCAGC---GCCGTGGCTGGCGGATGCGTAGC 12093  
QY 291 PheAlaArgProSerSerAlaAlaAlaLeuAlaPheValThrPalGlyLeuProGlnGly 310  
Db 12094 ATTCCGGCGGAGCGGTACACCTCT-----GCCGAATCCCGTAAAC 12135  
QY 311 GlyThrAlaPro-----Ala 315  
Db 12136 GTTACGCGATCCGGTACGCGTGCATCTCTCGCGCGTGGCGGTGAGCATCAACGCCATTACC 12195  
QY 316 GlyThrProAlaThrProGlnAlaSerSerGlyTyrLeuThrThrPheHisAlaGly 335  
Db 12196 GCCGATATGATGATCAACGCTGCCGAAAGCGCGCGGTAAAGCGCTCCGCGAGCAC 12255  
QY 336 ThrThrPheProAlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGluArg 355  
Db 12256 TCTGCGCTTGAAGCGCGCAACAACGTTACGCTACCTTTGGCGCGCAAACTTACAGCGCC 12315  
QY 356 TyrAspProAsnAspGlySerThrThrAspPheAlaSerAlaGlyAspThrValThrPhe 375  
Db 12316 ACGGTGGCTGCGAATGGTCTCTCGAGCAGCCTCGGCTCCGCGCGCATATGCGCGCTCTG 12375  
QY 376 Arg-----GlnValAlaValAspGluVal-----Val 384  
Db 12376 CGTATGCGCGATGCCAGCGCACGCGCATGTCAGCAATGTTAAAGCGCAACAGCGCCACC 12435  
QY 385 ValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrValArgValProPro 404  
Db 12436 ACGACCCACGCTTACAGCGTTGATGCGCAGCGCGCGCAACGCGTACATT----- 12483  
QY 405 SerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluThrArgProSerSer 424  
Db 12484 -----AATACCATTCGCGCGATGATGATTTCTTAACGCCCGCGCAAGCCGGA 12528  
QY 425 ArgArgLeuGluLeuPro---MetProProAlaAspPheGlyGlnThrValAlaAsnAsn 443  
Db 12529 GCGGCTGTGACCATCACCAGCGAGCAGCAGCGCGGAGCGGAGCGGAGCGGTG----- 12579  
QY 444 ProLysIleGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuValHisSerLys 463  
Db 12579 ----- 12579  
QY 464 MetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValSerPheAsn 483  
Db 12580 -----ACCGTCACGCTCAAT 12594  
QY 484 AsnProGlyTyrGluArgThr----- 490  
Db 12595 GGCACAACCTACACCGGACCGTACAGACGAGCGAGCTGGAGCGTCAAGCGTCA 12654  
QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMetSerThrAla 510  
Db 12655 GCCGACTTAAGCACCCTGACCGCGCAGCACTACACCGTGAACGCGGCGGTAGCGACAAA 12714  
QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGly 530  
Db 12715 GCCGAAACCGCGCTGGTTAATACACAACCTGACGGGTGATACGTCCGTT----- 12765  
QY 531 TyrPheGluValThrAsnValAsnThrProPheGly-----Gln 543  
Db 12766 -----CCGTCGTACCATCAACGCGTGGAGCGATGATGATCAACGCGAGGAA 12819  
QY 544 PheAlaHisAlaGlyLeuLeuLysAsnGluIleLeuCysLeuAlaAspAspLeuAla 563  
Db 12820 CACGCGCCAGCGGAGATCATAGCGGCTCCGCCACTGAGCGGCAACCGGTAGCACCGTG 12879  
QY 564 Thr-----ArgLeuThrGlyValTyrProAlaThrAspAsnPheAla 577  
Db 12880 ACGGTGACTATGCGACAATACTTATACACGGTGTGATGCCAGCGGCACTGAGAGC 12939

QY 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThr 597  
Db 12940 GTCCGCGTT-----CCGCGAAGCGTGTCTCGGCACTGGCGAATGGCAGCGTAC 12990  
QY 598 ---SerSerIleIleLysSerValGly-GluThrAlaValGlyAlaAlaGlnSerGlyLe 616  
Db 12991 ATCAATGCCAGCGTCAACCGATGCCGCGAGAAACAGCG----- 13027  
QY 616 ValAlaLysLeuProGlyLeuLeuMetSerValProGly----- 628  
Db 13028 -GCAGCGCTACCCATCAGTGCATGATGATACCGCGCTGCCAGCATTAACCTTAAAGCC 13086  
QY 629 -----LysIleAlaAl 632  
Db 13087 ATCAGCGCGGATTAACATCTGAACGCCGATGAAAAAGCCAGCGGTTGACCATCAGCGGC 13146  
QY 632 AlaGValArgAla---ArgArgAlaArgArgArgAlaAlaArgAla 646  
Db 13147 GCGAGTACGGGCGTGGCGAGCGGCGCGAGGTCAACGCTCAACGCTCA 13192

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Job time : 177 secs

